

0590
0730

#11



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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/781,693A

DATE: 08/12/2002

TIME: 14:11:56

Input Set : A:\11709-003001.TXT

Output Set: N:\CRF3\08122002\I781693A.raw

4 <110> APPLICANT: Chang, Tai-Jay
6 <120> TITLE OF INVENTION: ANDROGEN RECEPTOR COMPLEX-ASSOCIATED
7 PROTEIN
9 <130> FILE REFERENCE: 11709-003001
11 <140> CURRENT APPLICATION NUMBER: US 09/781,693A
C--> 12 <141> CURRENT FILING DATE: 2002-07-23
14 <150> PRIOR APPLICATION NUMBER: US 60/262,312
15 <151> PRIOR FILING DATE: 2001-01-17
17 <160> NUMBER OF SEQ ID NOS: 17
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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22 <211> LENGTH: 2580
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
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29 ttaaaacttg aagcaaccct taatgtgcat gatggttggtg ttaatacaat ctggttggaa 180
30 gacactggag aatatatatt atctggctca gatgacacca aattagtaat tagtaatcct 240
31 tacagcagaa aggttttgac aacaattcgt tcagggcacc gagcaaaca atttagtgc 300
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33 ttttatacca acgttgagca agatgcagaa accaacagac aatgccaatt tacgtgtcat 420
34 tatggaacta cttatgagat tatgactgta cccaatgacc cttacacttt tctctcttgt 480
35 ggtgaagatg gaactgttag gtggtttgat acacgcatca aaactagctg cacaaaagaa 540
36 gattgtaaaag atgatatttt aattaactgt cgacgtgctg ccacgtctgt tgctatttgc 600
37 ccaccaatac catattacct tgctgttggt tgttctgaca gctcagtacg aatatatgat 660
38 cggcgaatgc tgggcacaag agctacaggg aattatgcag gtcgaggacg tactggaatg 720
39 gttgcccggt ttattccttc ccatcttaat aataagtcct gcagagtgc atctctgtgt 780
40 tacagtgaag atggtcaaga gattctcgtt agttactctt cagattacat atatcttttt 840
41 gaccgaaaag atgatacagc acgagaactt aaaactcctt ctgcggaaga gagaagagaa 900
42 gagttgacgac aaccaccagt taagcgtttg agacttcgtg gtgattggtc agatactgga 960
43 cccagagcaa ggccggagag tgaacgagaa cgagatggag agcagagtcc caatgtgtca 1020
44 ttgatgcaga gaatgtctga tatgttatca agatggtttg aagaagcaag tgaggttgca 1080
45 caaagcaata gaggacgagg aagatctcga cccagaggtg gaacaagtca atcagatatt 1140
46 tcaactcttc ctacggtccc atcaagtcct gatttggaag tgagtgaac tgcaatggaa 1200
47 gtagatactc cagctgaaca atttcttcag ccttctacat cctctacaat gtcagctcag 1260
48 gctcattcga catcatctcc cacagaaagc cctcattcta ctctttgct atcttctcca 1320
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52 agtatagcat caagttctag aggaattggg agccattgca aatctgaggg tcaggaggaa 1560
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54 gaagaatcat cagaggatgt gacaaaatat caggaaggag tatctgcaga aaaccagtt 1680

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56 tcaggagaaa gaaatgacct caatcttgat cgctcttggt gggttccaga agaattctgct 1800
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58 aatgaaaata acaccaatcc tgagcctcag ttccaaacag aagccactgg gccttcagct 1920
59 catgaagaaa catccaccag ggactctgct cttcaggaca cagatgacag tgatgatgac 1980
60 ccagtcctga tcccagggtc aaggtatcga gcaggacctg gtgatagacg ctctgctgtt 2040
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62 actttgaaca ttagaaggcc gctagtaaaa atggtttata aaggccatcg caactccagg 2160
63 acaatgataa aagaagccaa tttctggggt gctaactttg taatgagtgg ttctgactgt 2220
64 ggccacattt tcattctggga tcggcacact gctgagcatt tgatgcttct ggaagctgat 2280
65 aatcatgtgg taaactgcct gcagccacat ccgtttgacc caattttagc ctcatctggc 2340
66 atagattatg acataaagat ctggtcacca ttagaagagt caaggatttt taaccgaaaa 2400
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72 <211> LENGTH: 860
73 <212> TYPE: PRT
74 <213> ORGANISM: Homo sapiens
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79 Arg Ser Leu Gly Leu Glu Asp Pro Ser Arg Leu Arg Ser Arg Tyr Leu
80 20 25 30
81 Gly Arg Arg Glu Phe Ile Gln Arg Leu Lys Leu Glu Ala Thr Leu Asn
82 35 40 45
83 Val His Asp Gly Cys Val Asn Thr Ile Cys Trp Asn Asp Thr Gly Glu
84 50 55 60
85 Tyr Ile Leu Ser Gly Ser Asp Asp Thr Lys Leu Val Ile Ser Asn Pro
86 65 70 75 80
87 Tyr Ser Arg Lys Val Leu Thr Thr Ile Arg Ser Gly His Arg Ala Asn
88 85 90 95
89 Ile Phe Ser Ala Lys Phe Leu Pro Cys Thr Asn Asp Lys Gln Ile Val
90 100 105 110
91 Ser Cys Ser Gly Asp Gly Val Ile Phe Tyr Thr Asn Val Glu Gln Asp
92 115 120 125
93 Ala Glu Thr Asn Arg Gln Cys Gln Phe Thr Cys His Tyr Gly Thr Thr
94 130 135 140
95 Tyr Glu Ile Met Thr Val Pro Asn Asp Pro Tyr Thr Phe Leu Ser Cys
96 145 150 155 160
97 Gly Glu Asp Gly Thr Val Arg Trp Phe Asp Thr Arg Ile Lys Thr Ser
98 165 170 175
99 Cys Thr Lys Glu Asp Cys Lys Asp Asp Ile Leu Ile Asn Cys Arg Arg
100 180 185 190
101 Ala Ala Thr Ser Val Ala Ile Cys Pro Pro Ile Pro Tyr Tyr Leu Ala
102 195 200 205
103 Val Gly Cys Ser Asp Ser Ser Val Arg Ile Tyr Asp Arg Arg Met Leu
104 210 215 220
105 Gly Thr Arg Ala Thr Gly Asn Tyr Ala Gly Arg Gly Thr Thr Gly Met

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106	225				230				235				240			
107	Val	Ala	Arg	Phe	Ile	Pro	Ser	His	Leu	Asn	Asn	Lys	Ser	Cys	Arg	Val
108					245					250					255	
109	Thr	Ser	Leu	Cys	Tyr	Ser	Glu	Asp	Gly	Gln	Glu	Ile	Leu	Val	Ser	Tyr
110				260					265					270		
111	Ser	Ser	Asp	Tyr	Ile	Tyr	Leu	Phe	Asp	Pro	Lys	Asp	Asp	Thr	Ala	Arg
112			275					280					285			
113	Glu	Leu	Lys	Thr	Pro	Ser	Ala	Glu	Glu	Arg	Arg	Glu	Glu	Leu	Arg	Gln
114		290					295					300				
115	Pro	Pro	Val	Lys	Arg	Leu	Arg	Leu	Arg	Gly	Asp	Trp	Ser	Asp	Thr	Gly
116	305					310					315				320	
117	Pro	Arg	Ala	Arg	Pro	Glu	Ser	Glu	Arg	Glu	Arg	Asp	Gly	Glu	Gln	Ser
118					325					330					335	
119	Pro	Asn	Val	Ser	Leu	Met	Gln	Arg	Met	Ser	Asp	Met	Leu	Ser	Arg	Trp
120			340						345				350			
121	Phe	Glu	Glu	Ala	Ser	Glu	Val	Ala	Gln	Ser	Asn	Arg	Gly	Arg	Gly	Arg
122			355					360					365			
123	Ser	Arg	Pro	Arg	Gly	Gly	Thr	Ser	Gln	Ser	Asp	Ile	Ser	Thr	Leu	Pro
124		370					375					380				
125	Thr	Val	Pro	Ser	Ser	Pro	Asp	Leu	Glu	Val	Ser	Glu	Thr	Ala	Met	Glu
126	385					390					395				400	
127	Val	Asp	Thr	Pro	Ala	Glu	Gln	Phe	Leu	Gln	Pro	Ser	Thr	Ser	Ser	Thr
128				405					410					415		
129	Met	Ser	Ala	Gln	Ala	His	Ser	Thr	Ser	Ser	Pro	Thr	Glu	Ser	Pro	His
130			420						425				430			
131	Ser	Thr	Pro	Leu	Leu	Ser	Ser	Pro	Asp	Ser	Glu	Gln	Arg	Gln	Ser	Val
132			435					440					445			
133	Glu	Ala	Ser	Gly	His	His	Thr	His	His	Gln	Ser	Asp	Asn	Asn	Asn	Glu
134		450					455					460				
135	Lys	Leu	Ser	Pro	Lys	Pro	Gly	Thr	Gly	Glu	Pro	Val	Leu	Ser	Leu	His
136	465					470					475				480	
137	Tyr	Ser	Thr	Glu	Gly	Thr	Thr	Thr	Ser	Thr	Ile	Lys	Leu	Asn	Phe	Thr
138				485					490					495		
139	Asp	Glu	Trp	Ser	Ser	Ile	Ala	Ser	Ser	Ser	Arg	Gly	Ile	Gly	Ser	His
140			500						505				510			
141	Cys	Lys	Ser	Glu	Gly	Gln	Glu	Glu	Ser	Phe	Val	Pro	Gln	Ser	Ser	Val
142			515					520					525			
143	Gln	Pro	Pro	Glu	Gly	Asp	Ser	Glu	Thr	Lys	Ala	Pro	Glu	Glu	Ser	Ser
144		530					535					540				
145	Glu	Asp	Val	Thr	Lys	Tyr	Gln	Glu	Gly	Val	Ser	Ala	Glu	Asn	Pro	Val
146	545					550					555				560	
147	Glu	Asn	His	Ile	Asn	Ile	Thr	Gln	Ser	Asp	Lys	Phe	Thr	Ala	Lys	Pro
148				565					570					575		
149	Leu	Asp	Ser	Asn	Ser	Gly	Glu	Arg	Asn	Asp	Leu	Asn	Leu	Asp	Arg	Ser
150			580						585				590			
151	Cys	Gly	Val	Pro	Glu	Glu	Ser	Ala	Ser	Ser	Glu	Lys	Ala	Lys	Glu	Pro
152			595					600					605			
153	Glu	Thr	Ser	Asp	Gln	Thr	Ser	Thr	Glu	Ser	Ala	Thr	Asn	Glu	Asn	Asn
154		610					615					620				

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157 His Glu Glu Thr Ser Thr Arg Asp Ser Ala Leu Gln Asp Thr Asp Asp
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159 Ser Asp Asp Asp Pro Val Leu Ile Pro Gly Ala Arg Tyr Arg Ala Gly
160                      660                      665                      670
161 Pro Gly Asp Arg Arg Ser Ala Val Ala Arg Ile Gln Glu Phe Phe Arg
162                      675                      680                      685
163 Arg Arg Lys Glu Arg Lys Glu Met Glu Glu Leu Asp Thr Leu Asn Ile
164                      690                      695                      700
165 Arg Arg Pro Leu Val Lys Met Val Tyr Lys Gly His Arg Asn Ser Arg
166 705                      710                      715                      720
167 Thr Met Ile Lys Glu Ala Asn Phe Trp Gly Ala Asn Phe Val Met Ser
168                      725                      730                      735
169 Gly Ser Asp Cys Gly His Ile Phe Ile Trp Asp Arg His Thr Ala Glu
170                      740                      745                      750
171 His Leu Met Leu Leu Glu Ala Asp Asn His Val Val Asn Cys Leu Gln
172                      755                      760                      765
173 Pro His Pro Phe Asp Pro Ile Leu Ala Ser Ser Gly Ile Asp Tyr Asp
174                      770                      775                      780
175 Ile Lys Ile Trp Ser Pro Leu Glu Glu Ser Arg Ile Phe Asn Arg Lys
176 785                      790                      795                      800
177 Leu Ala Asp Glu Val Ile Thr Arg Asn Glu Leu Met Leu Glu Glu Thr
178                      805                      810                      815
179 Arg Asn Thr Ile Thr Val Pro Ala Ser Phe Met Leu Arg Met Leu Ala
180                      820                      825                      830
181 Ser Leu Asn His Ile Arg Ala Asp Arg Leu Glu Gly Asp Arg Ser Glu
182                      835                      840                      845
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184                      850                      855                      860
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187 <211> LENGTH: 3016
188 <212> TYPE: DNA
189 <213> ORGANISM: Homo sapiens
191 <220> FEATURE:
192 <221> NAME/KEY: CDS
193 <222> LOCATION: (18)...(2597)
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198                      1                      5                      10
200 tgg gac gtg agg aaa agg tcc ctc ggg ctg gag gac ccg tcc cgg ctg          98
201 Trp Asp Val Arg Lys Arg Ser Leu Gly Leu Glu Asp Pro Ser Arg Leu
202                      15                      20                      25
204 cgg agt cgc tac ctg gga aga aga gaa ttt atc caa aga tta aaa ctt          146
205 Arg Ser Arg Tyr Leu Gly Arg Arg Glu Phe Ile Gln Arg Leu Lys Leu
206                      30                      35                      40
208 gaa gca acc ctt aat gtg cat gat ggt tgt gtt aat aca atc tgt tgg          194
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214	60	65					70					75					
216	gta	att	agt	aat	cct	tac	agc	aga	aag	gtt	ttg	aca	aca	att	cgt	tca	290
217	Val	Ile	Ser	Asn	Pro	Tyr	Ser	Arg	Lys	Val	Leu	Thr	Thr	Ile	Arg	Ser	
218	80					85					90						
220	ggg	cac	cga	gca	aac	ata	ttt	agt	gca	aag	ttc	tta	cct	tgt	aca	aat	338
221	Gly	His	Arg	Ala	Asn	Ile	Phe	Ser	Ala	Lys	Phe	Leu	Pro	Cys	Thr	Asn	
222	95					100					105						
224	gat	aaa	cag	att	gta	tcc	tgc	tct	gga	gat	gga	gta	ata	ttt	tat	acc	386
225	Asp	Lys	Gln	Ile	Val	Ser	Cys	Ser	Gly	Asp	Gly	Val	Ile	Phe	Tyr	Thr	
226	110					115					120						
228	aac	gtt	gag	caa	gat	gca	gaa	acc	aac	aga	caa	tgc	caa	ttt	acg	tgt	434
229	Asn	Val	Glu	Gln	Asp	Ala	Glu	Thr	Asn	Arg	Gln	Cys	Gln	Phe	Thr	Cys	
230	125					130					135						
232	cat	tat	gga	act	act	tat	gag	att	atg	act	gta	ccc	aat	gac	cct	tac	482
233	His	Tyr	Gly	Thr	Thr	Tyr	Glu	Ile	Met	Thr	Val	Pro	Asn	Asp	Pro	Tyr	
234	140	145					150					155					
236	act	ttt	ctc	tct	tgt	ggt	gaa	gat	gga	act	gtt	agg	tgg	ttt	gat	aca	530
237	Thr	Phe	Leu	Ser	Cys	Gly	Glu	Asp	Gly	Thr	Val	Arg	Trp	Phe	Asp	Thr	
238	160					165					170						
240	cgc	atc	aaa	act	agc	tgc	aca	aaa	gaa	gat	tgt	aaa	gat	gat	att	tta	578
241	Arg	Ile	Lys	Thr	Ser	Cys	Thr	Lys	Glu	Asp	Cys	Lys	Asp	Asp	Ile	Leu	
242	175					180					185						
244	att	aac	tgt	cga	cgt	gct	gcc	acg	tct	gtt	gct	att	tgc	cca	cca	ata	626
245	Ile	Asn	Cys	Arg	Arg	Ala	Ala	Thr	Ser	Val	Ala	Ile	Cys	Pro	Pro	Ile	
246	190					195					200						
248	cca	tat	tac	ctt	gct	gtt	ggt	tgt	tct	gac	agc	tca	gta	cga	ata	tat	674
249	Pro	Tyr	Tyr	Leu	Ala	Val	Gly	Cys	Ser	Asp	Ser	Ser	Val	Arg	Ile	Tyr	
250	205					210					215						
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253	Asp	Arg	Arg	Met	Leu	Gly	Thr	Arg	Ala	Thr	Gly	Asn	Tyr	Ala	Gly	Arg	
254	220	225					230					235					
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257	Gly	Thr	Thr	Gly	Met	Val	Ala	Arg	Phe	Ile	Pro	Ser	His	Leu	Asn	Asn	
258	240					245					250						
260	aag	tcc	tgc	aga	gtg	aca	tct	ctg	tgt	tac	agt	gaa	gat	ggt	caa	gag	818
261	Lys	Ser	Cys	Arg	Val	Thr	Ser	Leu	Cys	Tyr	Ser	Glu	Asp	Gly	Gln	Glu	
262	255					260					265						
264	att	ctc	gtt	agt	tac	tct	tca	gat	tac	ata	tat	ctt	ttt	gac	ccg	aaa	866
265	Ile	Leu	Val	Ser	Tyr	Ser	Ser	Asp	Tyr	Ile	Tyr	Leu	Phe	Asp	Pro	Lys	
266	270					275					280						
268	gat	gat	aca														

VERIFICATION SUMMARY

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L:471 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:487 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:526 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:541 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:578 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:593 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16